Final report

Advanced genetic evaluation tools and systems enabling faster and more valuable genetic gain in the red meat industries

Project code: L.GEN.1704

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Abstract

Genetic evaluations for beef cattle and sheep have supported high rates of genetic gain for these industries in Australia for up to 40 years, resulting in substantial contributions to the growth of the agricultural sector through productivity improvements and the development of new domestic and export markets. With livestock improvement entering the genomic era over the past decade, the evaluation systems required substantial upgrading to make use of this new source of information and capture the benefits of parallel industry investments in reference populations to support genomic selection. This new technology has allowed a much greater focus on improvement in breeding female efficiency and animal welfare traits to compliment long-term improvements already realised in production traits such as growth and carcase yield. Developments through this project has resulted in a seamless transition to the use of genomic data in the calculation of breeding values and associated information, for a greater range of traits supporting better breeding objectives. This research was driven by the needs of industry and supported by education and extension activities to aid seedstock breeders and buyers to capture the benefits, which are already being realised as increased rates of genetic gain in breeding objectives.

Executive summary

Background

Over the past 40 years, AGBU has worked with the Australian red meat industries to develop and implement genetic evaluation systems for beef cattle (since the mid-1970s) and sheep (since 1996). Building on these strong foundations, technology continues to change the face of modern breeding systems. To keep up with technological advances, genetic evaluation systems need development to make use of more data, whether phenotypic or genomic, in a timely manner, and provide better tools for breeders to make suitable selection decisions within an increasingly complex framework of information.

Objectives

1. Computation of Estimated Breeding Values in the era of genomics and big data – faster and more frequent analyses, with more data included. This objective was successfully met with systems and software developed and deployed in routine genetic evaluations for both sheep and beef, enabling use of rapidly expanding volumes of genomic data. In particular, single-step genomic evaluation was implemented and improved in the major sheep and beef evaluations, and a quality control pipeline for preparation of genotypes for BREEDPLAN single-step was developed.
2. Productivity gains were made possible through new on- and off-farm traits in key areas including efficiency and reproduction of breeding females, survival and disease resistance, meat yield, retail meat quality, and consumer eating quality. This objective was successfully met with new genomically enhanced breeding values for lamb meat quality and female reproduction in sheep, with the latter representing a major improvement in trait definition to separate components related to reproductive efficiency and welfare. In beef, genetic parameters for an expanded range of carcase traits for several breeds were estimated and introduced to BREEDPLAN, along with additional traits related to male and female fertility.
3. Maximising genetic gain through ongoing development of breeding objectives, integration of software for mating plans with genetic evaluation systems, and increased adoption through mentoring programs for genetics advisors and leading breeders. This objective was successfully met with the BREEDOBJECT system upgraded to incorporate significantly enhanced modelling of feed, along with capacity to include methane costs in breeding objectives and indexes for beef cattle. All the main breeds using BREEDPLAN have developed new indexes through the upgraded BREEDOBJECT. For sheep, important new indexes balancing eating quality and lean meat yield were introduced in terminal sire sheep and for dual-purpose maternal sheep.

Methodology

The work was conducted by:

- Consultation with MLA consultative committees, Sheep Genetics, ABRI, breed societies and other stakeholders, including breeders, identifying priority R&D questions or information needs.
- One or more members of the AGBU team would then work on solving the problem, and through internal review and presentation to external groups such as MLA managers, Sheep

Genetics, the Beef Technical Liaison Group, achieve feedback to improve approaches, leading to;

- Delivery of the appropriate result or tool(s) to ABRI and/or Sheep Genetics, or specific other stakeholders as appropriate
- Results were reported in scientific literature and industry communications events, where appropriate, in consultation with MLA

Workplans were developed and updated regularly in consultation with the relevant advisory and technical groups.

Key findings

The main technical developments include substantial improvements made to the analytical software used in BREEDPLAN and Sheep Genetics to seamlessly combine pedigree, performance and genomic data. More efficient computing strategies provide the basis for the rapidly expanding use of genomics. Improved breeding objectives and new traits for sustainable production of higher quality products, and better methodology to optimise breeding program design were developed. The outcomes of the project mean that beef and sheep seedstock breeders have access to the best tools possible for genetic evaluation, and that BREEDPLAN and Sheep Genetics continue to be world class and to provide accurate and useful information to breeders, commercial producers and other sectors of red meat value chains.

Benefits to industry

The advances in genetic evaluation methods and tools made in this project have led to substantial increases in genetic gain across a range of industry breeding objectives for sheep and beef. These improvements have contributed to improved enterprise profitability and productivity gains for the red meat industries.

Future research and recommendations

Although much progress has been made, further enhancements to BREEDPLAN and Sheep Genetics provide additional opportunities. As the size of genomic databases expands beyond millions of animals genotyped, new methodology for analysis and data management and greater investment in computing capacity will be necessary. Also, the trait emphasis of the future will continue to shift from production to more focus on traits related to resilience, environmental impact and others which will ensure a future strong social license for sheep and beef farming in Australia.

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1. Background

Over the past 40 years, AGBU has worked with the Australian red meat industries to develop and implement genetic evaluation systems for beef cattle (since the mid-1970s) and sheep (since 1996).

Genetic evaluation simply means estimating the value of animals' genes for traits we are interested in. These traits typically impact either income and/or cost at some point in the value chain. The outputs of genetic evaluation are estimated breeding values, called EBVs in beef cattle, and Australian Sheep Breeding Values (ASBVs) in sheep. Along with these core estimates, a range of other items of information relating to genetic merit have been developed, including selection indexes, inbreeding coefficients, genetic trend estimates, single gene tests, and more recently high-density marker genotypes used in genomic selection.

These estimates of genetic merit (EBVs or ASBVs) perform two fundamental functions:

- They allow accurate selection of the animals with the best genes for some defined purpose, typically involving multiple correlated traits. Selection is essential for genetic improvement, and accurate, relevant and reliable EBVs/ASBVs are essential to achieve high rates of genetic progress.
- They allow informed choice about which bull or ram to buy, and from which herd or flock. This means that commercial producers have information to underpin their purchasing decisions. In turn, this provides feedback and incentive to the breeders of bulls and rams, encouraging them to continue investing in performance recording and genetic evaluation.

The beef and sheep genetic evaluation systems developed and continuously updated by AGBU are unique in the world in their combination of several features:

- The genetic analyses are multi-trait, meaning that all information from traits that are influenced by the same genes are used in the estimation – making the estimated breeding values more accurate.
- The genetic analysis is multi-herd/flock, meaning that the EBVs and ASBVs in most cases allow comparison of animals across breeding herds/flocks and across time. This means breeders can accurately select and use the best animals from anywhere in the evaluated population. This in turn helps accelerate genetic progress and stimulates breeders to make better investment decisions to maintain competitiveness. In the case of sheep, maternal and terminal ram breeders can also compare animals across breeds.
- Multi-trait selection indexes have been produced for both species, either since the inception of the analysis, or not long after.
- Australia has led the world in the introduction of traits across the spectrum of production efficiency, product quality and animal health, where sufficient data is available to conduct the underpinning parameter estimation, and for traits that are relevant to Australian production systems.
- Overseas information, where available, is included in the analysis, meaning that Australian breeders can select animals from across the world with more confidence in their performance in Australian conditions.

- Genomic information has been introduced into multi-trait analysis in a cautious but accurate way. This includes ensuring that the accuracy estimates for genomic tests in Australia are calculated using independent Australian data.

Together, these features of the analysis, and their continued upgrading to introduce new traits, new and improved models for analysis, and improved computing strategies, are essential to ensuring both relevance and trustworthiness of genetic evaluations for beef cattle and sheep in this country. This is not to say that on its own this guarantees maximum uptake and utilisation: investment in the genetic evaluation system requires parallel investment in breeders,' commercial producers' and others' understanding of how to use the information generated and how it is best applied.

Without reliable, relevant genetic evaluation in Australia, rates of genetic progress are sure to be lower and less relevant. This is supported by evidence of the genetic progress being made before and after the introduction of BREEDPLAN, LAMBPLAN, MERINOSELECT (and the analogous systems in other species). Furthermore, without continual, relevant genetic progress, a livestock industry is quite literally continually going backwards in competitiveness.

The outcomes from this project will be essential to enabling industry to meet the following three goals of the MLA Genetics Business Plan:

- Increasing the rate of genetic progress.
- Ensuring that bull- and ram-buyers can make informed choices about genetic purchases.
- Ensuring that industry can utilise the resulting genetic information in production systems.

2. Objectives

The agreed objectives for this project were:

1. **Computation of Estimated Breeding Values in the era of genomics and big data – faster and more frequent analyses, with more data included**

    This project will integrate and develop the database systems, data processing pipelines, and genetic evaluation software necessary to support evaluation in this new era of "big data" in the red meat industries.

    This will allow potentially continuous evaluation of EBVs using genomic and phenotypic data collected with rapid turn-round at multiple points across the supply chain, enabling efficient genomically enhanced selection.

This objective was successfully met with systems and software developed and deployed in routine genetic evaluations for both sheep and beef, supporting use of rapidly expanding volumes of genomic data. Single-step genomic evaluation was implemented and improved in the major sheep and beef evaluations, and a quality control software pipeline for preparation of genotypes for BREEDPLAN single-step was developed.

2. **Productivity gains through new on- and off-farm traits**

    The key industry challenge in the coming decades will be to increase the rate of productivity gain in a more restrictive environment featuring increased input costs, the need to maintain sustained production under predicted climate changes, consumer demands for increased product quality, and societal requirements for ethical livestock production.

Meeting this challenge will require a greater focus on genetic improvement in several key areas, including efficiency and reproduction of breeding females, survival and disease resistance, meat yield, retail meat quality, and consumer eating quality.

In order to drive the necessary changes new economic traits will be incorporated into breeding objectives and EBVs for selection criteria will be developed, underpinned by genomic reference populations.

This objective was successfully met with new genomically enhanced breeding values for lamb meat quality and female reproduction in sheep, with the latter representing a major improvement in trait definition to separate components related to reproductive efficiency and welfare. In beef, genetic parameters for an expanded range of carcase traits for several breeds were estimated and introduced to BREEDPLAN, along with additional traits related to male and female fertility.

3. **Maximising genetic gain**

The third key component of this project is the design of cost-effective breeding programs which maximise genetic gain using the outputs of the genetic evaluation systems outlined in the first two objectives.

The basic tools for benchmarking performance across a suite of traits in different production systems and market environments are BREEDOBJECT and SHEEPOBJECT. Both will require ongoing development to evaluate new methods of defining economic values, to add new traits, and to expand delivery options, including for different users in different sectors of industry.

At the operational level of individual breeding programs, improved integration of software for mating plans with genetic evaluation systems will facilitate increased rates of genetic gain under the constraints faced by breeding businesses.

This objective was successfully met with the BREEDOBJECT system upgraded to incorporate significantly enhanced modelling of feed, along with capacity to include methane costs in breeding objectives and indexes for beef cattle. All the main breeds using BREEDPLAN have developed new indexes through the upgraded BREEDOBJECT. For sheep important new indexes balancing eating quality and lean meat yield were introduce in terminal sire and dual-purpose maternal sheep. Project staff conducted and participated in a wide range of adoption activities with advisors, breeders and breeder groups.

3. High performance genetic evaluation systems for sheep and beef

3.1 Sheep Genetics

AGBU has been responsible for the calculation of Australian Sheep Breeding Values (ASBVs) using the OVIS software system, delivered to industry by MLA’s national evaluation service Sheep Genetics through its MERINOSELECT and LAMBPLAN analyses.

The three largest Australian evaluations are for Merinos (MERINOSELECT), terminal sire breeds and maternal breeds (LAMBPLAN), and during this project all these evaluations were transitioned to “single-step” genomic analyses. Including these evaluations, ASBVs have been calculated fortnightly for eight Australian breeds or breed groups, and five international breed groups. Evaluations for all breeds have been performed fortnightly without interruption throughout the life of this project.

AGBU has also provided diagnostic support to Sheep Genetics in the form of automated comparisons of analysis outputs across time, on-line tools to decompose information sources contributing to ASBVs, and regular interaction between staff and breeders.

At the conclusion of this project Sheep Genetics' largest evaluations include more than 3.3M pedigree animals for Merino and terminal sire breeds, and up to 20.6M records across 94 traits in Merinos (Table 1). There has been considerable growth in the Merino evaluation, with the number of animals added by year of birth increasing from 150K in 2016 to 202K in 2020 (**Figure 1**). Terminal sire and maternal breeds have remained relatively constant over the same period, with around 130K and 70K animals added per year, respectively.

Numbers of genotyped animals have increased, particularly for Merinos with 159.2K in October 2021, and 51.3K and 35.4K for terminal and maternal breeds, respectively. Most of these genotypes have entered the analysis following the introduction of single-step in 2016/17 (**Figure 1**) and have been processed via genomic pipelines established first by the Sheep CRC, and from 2018 maintained by MLA project L.GEN.1903. Close collaboration between the respective genomic pipeline projects and single-step evaluations on quality control and rules to include genotypes in analyses ensures the integrity of ASBVs.

Table 1: Counts of animals in the pedigree, records, traits, genetic groups, and genotypes included in SS-GBLUP analyses for the three largest Sheep Genetics evaluations in October 2021

October 2021	Merino	Maternal	Terminal
Pedigree	3.3M	2.5M	3.5M
Records	20.6M	6.6M	10.8M
Traits	94	64	48
Genetic Groups	630	102	90
Genotypes	159.2K	35.4K	51.3K

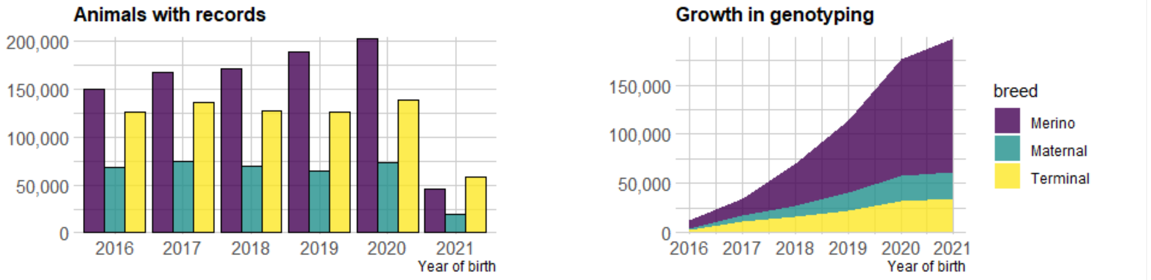

Figure 1: Growth in recorded animals and genotyping in Sheep Genetics Merino, maternal and terminal sire breed evaluations between 2016 and October 2021

In addition to routine delivery of ASBVs, the OVIS software was continually improved and updated with the R&D outputs from this and other projects. Major updates to OVIS were made once per year in quarter 2 (April – June) and are summarised in **Table 2**. A feature of the R&D has been collaboration to incorporate the outcomes of external projects into OVIS, for example including the Sheep CRC (Flock Profile, updated marker panel with predictive SNPs) and MLA projects including the Resource Flock (carcase and eating quality traits), L.GEN.1903 (genomic pipeline), and L.GEN.2004 (Data Quality Score).

Table 2: annual upgrades to Sheep Genetics evaluations introduced through L.GEN.1704 and collaborative R&D programs

2017	• Single-step genomic evaluations implemented fully in Merino, terminal sire and maternal breeds for the main analyses as well as visual trait, and worm egg count sub-analyses • Improved filtering of data in reproduction analyses
2018	• Performance enhancements to OVIS software pipeline to reduce analysis run times • Standardisation of genomic information used across main and sub-analyses within each evaluation • Implementation of the Flock Profile genomic benchmarking system for commercial Merino flocks • Updated Maternal$ index for maternal breeds
2019	• Multi-breed genomic evaluation introduced for terminal sire and maternal breed analyses • Single-step Research Breeding Values (RBVs) for reproduction component traits for maternal breeds • Replacement of Carcase Plus with a new Terminal Carcase Production index (TCP) for terminal sire breeds • Introduction of a Maternal Wool Production index (MWP+) for Corriedale breeders • New methods for describing standard indexes adopted • Diagnostic tool to use genomic data to test parent-offspring relationships • OVIS components updated to use the Python 3 programming language
2020	• Updated SNP marker panel with inclusion of Sheep CRC predictive SNPs in single-step analyses • Scaling of genomic and pedigree relationships in Merino single-step analyses • Single-step RBVs for reproduction component traits for Merinos • Footrot breeding values for New Zealand Merinos • Worm egg count Flock Profile predictions • Improved solver performance and calculation of ASBV accuracies • Inclusion of AWI Merino Lifetime Productivity data in Merino analyses
2021	• New computer server commissioned resulting in substantially improved performance and timeliness of results • Reproduction component trait analyses for maternal breed and Merino analyses transitioned from RBV to ASBV status • Introduction of the Data Quality Score (DQS) system developed in MLA L.GEN.2004

Starting in 2019 Sheep Genetics began a major upgrade of its database system supporting sheep pedigree, performance, and genomic data from breeder and research flocks. Prior to the upgrade the system comprised separate databases for different breed groups based on outdated technology platforms, posing some risks to Sheep Genetics and MLA.

The Sheep Genetics Database Re-development Project was initiated to address these risks, future-proof genetic evaluations and genetics RD&E. AGBU has and will continue to play a key role in the re-development, which represents one of the most important changes in the history of Sheep Genetics.

3.2 BREEDPLAN

Beef genetic evaluations for Australia are conducted using BREEDPLAN software developed by AGBU and licensed to ABRI who run the analyses on behalf of breed societies. ABRI runs evaluations for Australian societies as well as for international clients.

The major development for BREEDPLAN during this project has been the implementation of single-step evaluations for the Angus, Brahman, and Hereford breeds in 2017, Wagyu in 2018, and recently for Santa Gertrudis. The scale of the main evaluations with changes between January 2018 and November 2021 are shown in Figure 2, detailing the increases in the number of genotyped animals in the five breeds through this period. Angus and Wagyu have increased most with 176K and 89K genotypes in November 2021 single-step evaluations, respectively, with Hereford and Brahman showing slower growth (39K and 34K genotypes), and Santa Gertrudis only recently switching to single-step (6K genotypes).

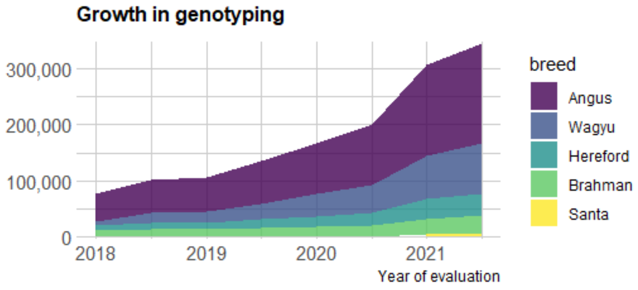

Figure 2: Growth in number of genotypes included in BREEDPLAN single-step evaluations

Single-step evaluations for Brahman, Hereford, Wagyu cattle and Santa Gertrudis are being run at monthly intervals, while Angus have been run at bi-monthly intervals for the last 48 months. Implementation of single-step requires updating of pedigree from new extracts and constructing genomic relationship matrixes (G matrixes) for each breed. With each (bi)monthly update across the five breeds, comprehensive G matrix diagnostic reports are produced and delivered to ABRI. These diagnostic reports include quality of genotypes, breed composition, and mismatch of recorded pedigree and genomic pedigree, and provide recommendations regarding responses to each type of error.

In addition to the implementation of single-step a range of other enhancements and updates to BREEDPLAN evaluations and BREEDOBJECT indexes were introduced during L.GEN.1704, as shown in **Table 3**.

Table 3: upgrades to BREEDPLAN evaluations introduced through L.GEN.1704

2016	• Release of BREEDOBJECT V6
2017	• Establish SNP manifests, haplotype libraries, allele frequencies, and quality controls for single-step genomic pipeline. • Single-step implemented in Brahman, Hereford, and Angus • US EPD information updated into the evaluation of Angus and Shorthorn evaluations • Software update for BREEDOBJECT

2018	- New docility evaluation for Shorthorn cattle from the Performance Herds of Australia (PHA) - New calving ease evaluation for South Devon cattle - New genetic parameters and adjustment factors implemented for Wagyu cattle - Multi-breed single-step evaluation introduced for Brahman, Droughtmaster and Santa Gertrudis cattle using *Repronomics*^{TM} data - Wagyu V6 indexes released - Single-step implemented in Wagyu
2019	- Hereford V6 indexes released - Version 7 genomic pipeline implemented for Wagyu and Angus - New genetic parameters and adjustment factors implemented for Shorthorn cattle from PHA - New dam age adjustment included for gestation length evaluation of Angus, Brahman, Charolais, Hereford, Limousin, Shorthorn and Simmental
2020	- Genomic pipeline updated with dam discovery, identical twin inclusion, and enhanced diagnostics for handling exceptions - GTBLUP implemented in single-step BREEDPLAN to accommodate breeds with large numbers of genotypes, such as Angus at this point - Limousin V6 indexes released - Version 8 genomic pipeline implemented for Wagyu and Angus - Pre-pipeline genomic diagnostics software developed to allow timely information to clients - US and Canadian EPD information incorporated into the Simmental and Red Angus evaluations
2021	- Single-step implemented in Santa Gertrudis - Single-step tested and ready for implementation in Australian Charolais - Angus EBV information incorporated into the evaluation of Simmental cattle - US and Canadian EPD information updated into the Hereford evaluation - Charolais and Belmont Red V6 indexes released - Version 8 genomic pipeline implemented for Hereford - Commercial genomic pipeline software (and pre-pipeline genomics diagnostics software) delivered to ABRI.

3.3 Advanced data processing software for genetic evaluation

The OVIS and BREEDPLAN software systems are capable of processing large volumes of data at high speeds with efficient use of computing resources. At the heart of these systems is the “solver” software used to apply sophisticated statistical models to calculate multi-trait genomic breeding values. The AGBU solver software underwent several major upgrades during L.GEN.1704 to support the expansion of genomic data. This included a complete ground-up re-write to provide substantially greater performance and flexibility in model fitting, including random variables with a greater range of (co)variance structures, and the ability to directly include adjustments for any combination of systematic environmental effects, negating the need for pre-analysis adjustment procedures typically used. These features have been applied in several new analyses for reproduction and lambing ease in sheep (Sections 0 and 0) and calving ease in beef (Section 0). In addition, high performance algorithms to support large numbers of genotyped animals have been implemented (see Section 0), ensuring the sustainability of single-step evaluations into the future.

4. Single-step genomic evaluation

Single-step genomic evaluations have become a key component of integrating genomic selection in industry evaluation programs where only a small proportion of animals in the analysis are genotyped.

The sheep and beef cattle industries in Australia have made significant investments to develop reference populations to facilitate the implementation of genomic selection. Animals in these populations have been genotyped with high-density SNP panels, and extensively recorded for hard-to-measure traits. These reference populations underpin genomically enhanced breeding values available to breeders via Sheep Genetics and BREEDPLAN evaluations. Traits are directly related to economic merit and include carcass traits, reproduction, disease resistance, and feed efficiency.

Genomic evaluations based on these reference populations have been performed in the two industries over the last decade, initially using simple “blending” methods of combining genomic and pedigree breeding values from separate analyses, and delivered to breeders as Research Breeding Values (RBVs) (Swan et al. 2012). Efficient single-step methods described by Aguilar et al. (2010) and combining all sources of information in a single analysis were then developed for Australian sheep and beef in 2016 within MLA projects B.SGN.0127 and B.BFG.0050 (Swan et al. 2016).

Full implementation in Sheep Genetics and BREEDPLAN was achieved within L.GEN.1704 in 2017. Subsequent R&D lead to improvements in computing times for both breeding values and accuracies, along with new knowledge and applications of single-step, described in the following sections.

4.1 BREEDPLAN genomic pipeline

The BREEDPLAN genomic pipeline was first developed in 2015 to handle genomic data for single-step-evaluations. It requires raw genotypes and BREEDPLAN pedigree extracts as input and through several steps it generates the genomic data required for single-step BREEDPLAN. The pipeline ensures genomic data entering BREEDPLAN is of sufficient quality through applying several quality control checks. These include genotype quality checks, duplication, and pedigree alignment (parent verification, sex verification), along with parent discovery. Importantly genotypes must meet requirements for relationship to the genomic population (formally referred to as breed composition). Genotypes that fail quality control are excluded from the evaluation and are reported back to BREEDPLAN users with diagnostics providing reasons for failures, enabling breeders to investigate and correct the issues. These procedures ensure reliable use of genomic information in single-step evaluations, providing accuracy and stability which facilitates adoption and trust from users.

The genomic pipeline has been improved throughout this project through a series of software updates, along with annual updates to pipeline elements for each breed evaluation, namely allele frequencies, SNP inclusions, and the haplotype reference library. These three elements are estimated from the whole population and for all genomic products each year, and are fixed until the next annual update, ensuring EBV stability between runs but also keeping the system current over time, by capturing new information added during the previous year. The pipeline software has undergone extensive automation and has been delivered to ABRI for use in their computing environment.

A standalone version of the pipeline software has also been developed. This software performs all the diagnostic quality control procedures that currently exist in the BREEDPLAN pipeline, and provides the same diagnostic output, without the extensive process of generating the genomic data inputs for BREEDPLAN. This software was designed for simple application on any animal (registered/unregistered), for any provided SNP extract. This enables BREEDPLAN diagnostics to be performed outside the scheduled BREEDPLAN timelines, meaning BREEDPLAN clients have access to parent verification, parent discovery, and other diagnostics, earlier than their monthly evaluations. This enables breeders access to diagnostic information early, for example, to obtain new DNA samples for poor quality genotypes, or for parentage in calf registration. This software was delivered to ABRI as BREEDPLAN support software and has potential as a tailored commercial standalone DNA service.

The number of new genotypes per year is now approximately equal to half the annual throughput of BREEDPLAN in Australia. The quality control of genotypes ensures increased accuracy of EBVs given the data available, and just as importantly, minimal corruption due to contaminated samples, poor reads, labelling and other handling errors. Single-step would not be as well accepted without these checks and edits, but it is worth noting that exclusion rates have been averaging less than 4% across breeds, and typically less than 1%.

4.2 Estimation of genomic breed composition

An early realisation made in this project was that animals from multiple breeds would be routinely genotyped by breeders and in reference populations. Determining breed composition from genomic information is invaluable for genomic evaluations, both for quality control of genotypes in single breed evaluations and as an essential analysis component in multibreed evaluations (see Section 0). A method was therefore developed to estimate breed proportions based on allele frequencies for each population observed in a reference set of genotyped animals (Boerner and Wittenburg 2018). Given adequate representation of all reference breeds the method will also estimate fractional contributions in crossbred and composite animals. A software tool implementing the method was developed.

This tool is used in the beef genomic pipeline for the single-step analyses performed for each breed, to ensure genotypes included in the evaluation are sufficiently related to the main breed being analysed. The BREEDPLAN genomic pipeline requires imputation for missing SNPs and consolidation of many different genomic products to a common SNP density for the evaluations. As such, imputation requires breed-specific genomic data for sufficient accuracy, and the breed proportion algorithm estimates whether individuals are sufficiently related to the main breed’s genomic population, and therefore can be included in the evaluation and used for imputation. Implementation of this quality assurance step has led to considerable engagement with breeds and breeders about the meaning of test results, especially around the concept of "breed". This has been challenging but worthwhile, in that it ultimately increases focus on the quality of the reference population i.e, the genotyped animals with data.

For the sheep analyses, research was conducted into determining which breeds were genomically represented in the genotypes available and for which breeds breed composition could be calculated (Gurman et al. 2017). This list of breeds has expanded and now covers four strains of Merinos (required for prediction due to the genomic diversity in the Merino breed), Border Leicester, Corriedale, Hampshire Down, Southdown, Coopworth, Poll Dorset, Texel, White Suffolk, Dorper, South African Meat Merinos (SAMM) and Dohne Merinos. These breed proportion estimates are used for multiple purposes, most importantly the calculation of the expected allele frequency for each animal in breed adjusted genomic relationship matrices (Section 0).

4.3 Importance of aligning genomic and pedigree relationships

Single-step accounts for genomic information using genomic relationships between animals based on marker genotypes, which are then "imputed" to animals without genotypes via pedigree relationships. In typical data structures the bulk of the genotypes are from the current generation, while the pedigree extends back several generations to the founder animals.

An important finding in this project was that this type of data structure can result in apparent loss of genetic trend, because the base animals for genotyped and pedigree-only animals are not aligned (Meyer et al. 2018).

Correct estimation of genetic trend is critical for benchmarking genetic progress and accurate comparisons of breeding values across generations. Consequently, aligning pedigree and genomic relationships in single-step is essential. The most effective solution to this problem is to fit "meta-founders" (Legarra et al. 2015), but simple scaling procedures can also be used.

A significant loss of genetic trends was observed in a large Merino flock which genotyped essentially all progeny in 2018 and 2019 (6.6K genotypes in total). Scaling of the genomic relationship matrix (G) to the pedigree relationship matrix (A) was then implemented in the Merino analysis, using the scaling approach described by Christensen (2012).

The long-term solution is to move to meta-founder analyses, which can also address issues related to unknown parent genetic groups (Meyer 2021). However, due to the large number of genetic groups without genomic information in the Merino analysis, application of meta-founders is not straightforward. In the interim, the Christensen scaling method has proven effective for this analysis.

4.4 Multibreed genomic evaluations in sheep

Terminal sire and maternal breed sheep evaluations are strongly multibreed, with the major breeds Poll Dorset, White Suffolk, Dorper, Border Leicester, Coopworth and Corriedale complimented by significant contributions from smaller breeds such as Suffolk, Dorset, Texel, and Hampshire. Demand for these combined analyses is driven by the desire of breeders to compare animals across breeds, with few organisational impediments to using sires from different breeds in breeding programs. This has led to high levels of admixing of breeds across the population, and the formation of important terminal and maternal composite flocks.

The genomic relationships used in these evaluations account for breed structure by scaling marker genotypes by allele frequencies estimated for each breed, also incorporating genomic breed composition information for crossbred and composite animals (Gurman et al. 2019). This requires suitable reference populations for each breed for accurate imputation and estimation of breed composition which can be a challenge for small breeds. Information from evaluations has been used for targeted genotyping of underrepresented breeds through the Sheep CRC and MLA Resource Flock project (MLA L.GEN.1814).

Improvements due to using this multibreed approach, compared to assuming all genotyped animals originate from a single population, include:

- Small increases in validation accuracy and reduction in bias.
- Improved estimation of genetic trends because the multibreed approach leads to better alignment of genomic and pedigree relationships, the importance of which is discussed in Section 0.

- Breeding value accuracy approximations can be inflated, especially for under-represented breeds.

Alternative methods for multibreed genomic evaluation are an area of active research, with the meta-founders approach again showing promise (Meyer and Swan 2019). In principle these methods are equally applicable in both sheep and beef, and a common approach is possible.

4.5 Flock Profile genomic benchmarking of commercial Merino flocks

Flock Profile is a genomic tool used to benchmark commercial Merino flocks, developed by AGBU in collaboration with the Sheep CRC. Genomic predictions are made on genotypes from a random sample of commercial flock animals, and then averaged to derive a mean breeding value on the scale of ASBVs (Swan et al. 2018). A key feature of the method is approximation of genetic group differences between flocks through genomic relationships, with validations showing accuracies of predicting flock means averaging 0.82 for key economic traits (ranging between 0.67 and 0.93).

Flock Profile was first released in 2018, including benchmarks for wool, body weight and body composition traits as well as overall index profitability. In 2020 worm egg count predictions were added.

The methodology developed for Flock Profile has scope for other applications, including efficient computation of genotype-only breeding values in both species.

4.6 Marker panels including predictive SNPs for sheep traits

On most marker panels used in livestock improvement SNPs are chosen to ensure good coverage of the genome with uniform distributions of allele frequencies, without targeting specific QTL. Reductions in the cost of genome sequence combined with accurate imputation methods mean that it is now possible to conduct full Genome Wide Association Studies (GWAS) to find predictive SNPs for economic traits.

Research conducted by the Sheep CRC led to the development of a set of around 5000 predictive SNPs for carcase and eating quality traits, which were then commercialised by Neogen on their GGP Ovine 50K product. These markers were incorporated in the “union” set used for single-step sheep evaluations in 2020. Validation studies have shown small increases in genomic prediction accuracy when the predictive SNPs are included with all SNPs in a single genomic relationship matrix (Li et al. 2021b).

This research has continued in parallel with this project in MLA L.GEN.1815, with updated sets of predictive SNPs for reproduction and carcase and eating quality traits due in 2022.

4.7 Single-step computation with many animals genotyped

In its original formulation single-step was a simple modification of traditional pedigree-only models for calculation of breeding values. However, computational demands have increased substantially because of the sheer volume of data generated by genomic testing: use of a 50K SNP panel in single-step equates to 50K additional data points for every animal genotyped relative to pedigree-only models. The parallel processing capabilities of modern computers have enabled efficient single-step evaluations, but as the number of animals genotyped increases beyond 150-200K, compute times increase to the point where weekly or fortnightly evaluations become unsustainable.

A new single-step algorithm which becomes advantageous when the number of animals exceeds the number of SNP markers, known as “single-step TBLUP”, has been developed by Mäntysaari et al. (2017). TBLUP was incorporated in OVIS and BREEDPLAN breeding value estimation software within L.GEN.1704, and an analogous TBLUP-like approach is under development for the calculation of breeding value accuracies. Two evaluations reached the point in 2020/21 where TBLUP is required due to growth in genotyping: the Angus BREEDPLAN and Merino Sheep Genetics analyses. The Angus evaluation changed to TBLUP in 2020, while the Merino evaluation is due to switch over in 2022.

Implementation of TBLUP has ensured the turn-around times of regular evaluations will be sustainable for the medium term, and methodology for calculating genotype-only breeding values post-analysis such as Flock Profile (Section 0) will be feasible. However, as the size of genomic databases expands beyond millions of animals genotyped, new methodology for analysis and data management and greater investment in computing capacity will be necessary.

4.8 Weighting of pedigree and genomic variation

Single-step combines genomic and pedigree information, with “imputation” from genotyped animals to their ungenotyped relatives in their pedigree, but additionally there are often parts of the data which do not have pedigree links to the genomic reference. The appropriate relative weightings to place on pedigree and genomic relationships is a requirement of single-step. The R&D leading to the implementation of single-step in OVIS and BREEDPLAN determined equal weighting was appropriate due to an increasing degree of bias in breeding values and a plateau in accuracy improvement with higher weightings on genomic information (McMillan and Swan 2017; Gowane et al. 2019).

The assumption of equal weighting has been continued for OVIS and BREEDPLAN evaluations to the present. However, more recent R&D within this project has suggested that as the size of reference populations has increased, more weight can be placed on genomic information for a number of traits in Angus cattle (Zhang et al. 2018; Samaraweera et al. 2021; Torres-Vázquez et al. 2021). Similar observations have been made for carcase traits in sheep within L.GEN.1815 (Gurman et al. 2021).

Maintaining up-to-date covariance parameters is a fundamental requirement of genetic evaluations, and in this context, further research is required on the appropriate weighting of pedigree and genomic information across a range of sheep and beef breeds and traits.

5. Productivity gains through new and improved traits and analyses

The development of new traits is an important component of improving genetic evaluation systems, along with updating models for existing traits. New traits contribute to increased genetic progress through better specification of breeding objectives, while regular revision of trait models including updated genetic parameters and adjustment factors ensures the predictive ability of breeding values as evaluation data changes. The growth of reference populations and genomic data has also influenced the development of new and existing traits. R&D conducted within L.GEN.1704 has led to major advances in the development of new traits in sheep and beef, and in ensuring confidence in breeding values for existing traits.

5.1 Genomic selection for lamb eating quality

Genetic improvement made possible through LAMBPLAN over a 30-year period achieved substantial gains in productivity and product quality, meeting demand by consumers for larger, leaner lambs and enabling expansion into international markets. A simple breeding objective focusing on growth and lean meat yield contributed to this rapid progress.

The reference population established by the Sheep CRC from 2007 to 2011 and continued as the MLA Resource Flock enabled the study of a greater range of carcase and eating quality traits than was previously possible. New understanding of genetic relationships revealed that long-term selection on growth and lean meat yield would lead to declining eating quality (Mortimer et al. 2018), a phenomenon observed in other species such as pigs. Lamb eating quality from consumer preference data was heavily influence by intramuscular fat (marbling) and shear force (tenderness) and these traits have genetic antagonisms with lean meat yield.

Meat and eating quality traits are expensive to measure, and direct measurement is not possible on selection candidates. As such, they are ideal candidates for genomic selection. The full implementation of single-step for LAMBPLAN evaluations within this project, with breeding values for carcase and eating quality traits underpinned by reference populations recorded for carcase traits, and new indexes which balance selection for growth and lean meat yield with eating quality (Swan et al. 2015) have allowed breeders to reverse declining lamb eating quality while maintaining productivity gains. Genetic trends for the White Suffolk breed in **Figure 2** show that since around the time of introduction of single-step in 2017, increases in intramuscular fat (IMF) and reductions in shear force (SF5) have contributed to improvements in consumer eating quality (MSA) while maintaining strong gains in growth (PWT) and lean meat yield (LMY).

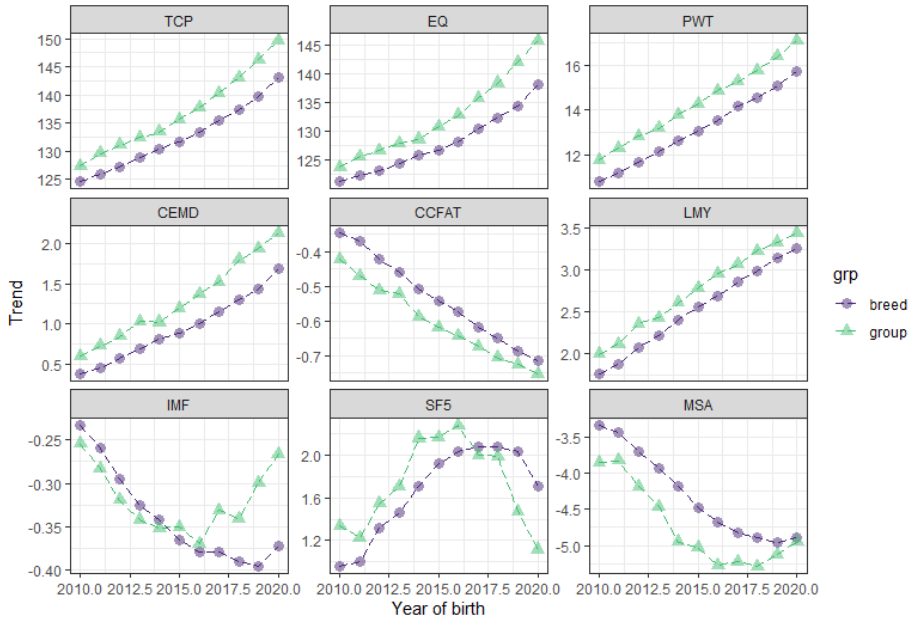

Figure 2: LAMBPLAN genetic trends in TCP and EQ indexes and key economic and index traits for a White Suffolk breeder group versus the entire breed.

This example demonstrates the transformative power of genomics underpinned by well-designed reference populations and advanced selection tools developed and implemented within L.GEN.1704. To date breeders have made these changes to their breeding objective with the future vision that producers will receive price signals for superior eating quality. AGBU have activity been collaborating with the ALMTech project to capture objective measurements from the supply chain to inform both value-based pricing/market and the genetic evaluation where appropriate. This has also involved collaboration with the MSA sheep meat pathways team which will be critical for wider adoption of balanced breeding objectives for lean meat yield and eating quality.

5.2 New sheep reproduction traits to improve ewe efficiency and welfare

A major achievement has been a complete modernisation of sheep reproduction analyses. The central feature of the update has been the definition of new traits targeting each stage of the reproductive cycle from joining to lambing and onto weaning. The three traits are:

- Conception (ewes pregnant per ewe joined)
- Litter size (lambs born per ewe lambing)
- Ewe rearing ability (proportion of lambs weaned per lambs born)

These traits address both reproductive efficiency and welfare and are available as both yearling and adult traits of ewes. To date the improved analyses have been applied in Merino and maternal breed analyses, replacing existing analyses based on the net reproduction trait number of lambs weaned per ewe joined (NLW). Critically, the new traits allow breeders to place emphasis differentially on each stage of the reproductive cycle. For example, conception may be the key trait in yearling ewes, and ewe rearing ability may require greater emphasis in flocks where mean litter size is already high. The capacity to focus on individual components is likely to become increasingly important as overall reproduction rate rises, and community focus on welfare issues (including lamb survival) intensifies.

Development of the new analysis system was a major undertaking from the ground up, featuring a completely new data preparation pipeline, model development, and implementation of single-step breeding values. The R&D has been described in detail by Bunter et al. (2019b), Bunter et al. (2019a), and Bunter et al. (2020), with key features including:

- Implementation of single-step
- Greater efficiency of data usage and improved filtering procedures compared to the previous analysis
- Better models for each trait, with a phasing out of pre-analysis adjustments in favour of fitting effects directly in the analysis
- Inclusion of male fertility traits (scrotal circumference) providing useful correlated information to improve female reproduction
- New breeding values for maternal behaviour, favourably related to ewe rearing ability and subsequently lamb survival
- New breeding values for pre-joining condition score
- Inclusion of data on body weight and composition (muscle and fat), predominantly to improve the accuracy of condition score breeding values

The new breeding values have improved predictability relative to NLW and have been well received by breeders to date. In addition, breeding values for a comparable composite trait (net weaning rate) can be derived from the component trait breeding values (Swan and Bunter 2021), if required.

Critically, the success of this new system was reliant on obtaining more detailed information from breeders through the development of a “mating module” recording system incorporating mating dates, pregnancy scan data, and information on event outcomes. Increased attention to recording reproductive data directly demonstrates a greater appreciation for the importance of reproduction by breeders.

Genetic trends for component traits and net weaning rate in **Figure 3** demonstrate how gains in individual traits combine to improve overall reproductive performance in net weaning rate, and from the comparison between the high performing flock relative to the breed average, that there is great potential to improve reproductive performance across the industry.

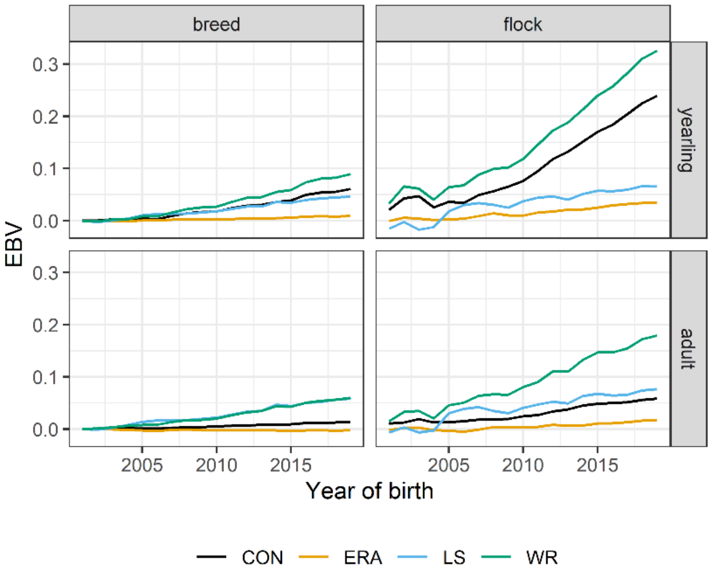

Figure 3: genetic trends in yearling and adult sheep reproductive component traits conception (CON), litter size (LS), ewe rearing ability (ERA), and net weaning rate (WR) for a maternal breed and a high performing flock within the breed.

The next steps in this research involve integration of reproduction component traits in the broader evaluation system, including re-development of indexes to value components directly. This will also require studies to establish genetic associations with other economic traits. The first of these studies focused on reproduction – wool trait associations in Merinos (Bunter and Swan 2021) but more will be required.

In addition, the new analysis will be developed for other evaluations beyond Merinos and maternal breeds, with possible extensions including the capacity to model accelerated lambing systems.

5.3 Advances in BREEDPLAN reproduction evaluations

Significant development of the current BREEDPLAN evaluation of reproduction traits has been a major activity in this project. New male and female traits have been investigated and their utility as standalone EBVs, or as predictors of genetic variation in the current descriptor of female reproductive performance (days to calving), have been explored, with the goal of transitioning to a new model for evaluating and describing genetic merit for female reproductive performance. This research is ongoing, and at the same time there is a clear need to simplify the reporting of genetic merit for reproduction in the BREEDPLAN evaluation. For this reason, transitioning to a single female conception, calving, or weaning rate EBV is under consideration with expected benefits to parallel what has been observed in sheep. The following have been investigated as potential contributors to the new description of genetic merit for female reproductive outcomes:

- **Calving rate from yearling mating in Brahmans for BREEDPLAN genetic evaluation:** Currently the BREEDPLAN genetic evaluation for days to calving (DC) in Brahmans excludes the mating records from yearling mating. This was required to avoid issues with low numbers of records and commonly low calving rates observed in this class of females, and its impact on the variance component estimates for DC. A study was initiated to develop a “trial” EBV for the calving rate from yearling mating (YCR) in Brahmans. The estimated heritability for YCR using a linear model was 0.16, and trial EBVs for sires with daughters in the dataset ranged from -25 to +26%. Brahman breeders have been encouraged by these first results to continue to record and submit records for yearling mated heifers. This trait is biologically equivalent to conception of yearling ewes, reported earlier, which has proven to have predictive capacity. However, care will be required to integrate this trait with age at puberty in the existing evaluations for beef cattle.
- **Relationship between percentage normal sperm and early and lifetime female reproductive performances:** Genetic relationships between percentage normal sperm (PNS) and early lifetime reproductive performance of females were investigated for Brahman (BRAH) and Santa Gertrudis (SANTA) (Jeyaruban and Johnston 2017). Genetic parameters for PNS and scrotal circumference (SC), and their genetic relationships with days to calving for first (DTC1) and second (DTC2) mating outcomes and the current, combined trait (which includes a maximum of six repeated records) (DTC_{all}) were estimated for BRAH and SANTA. Results showed that PNS and SC measured at 18 to 24 months of age in young BRAH and SANTA bulls were moderately heritable and their genetic correlations with DTC were favourable, and in the same direction for both breeds. PNS and SC had higher genetic correlations with early DTC measures compared to DTC measured across a female’s entire reproductive life, indicating that they may be more related to early reproduction than lifetime reproduction. In addition, PNS was more strongly related with all DTC measures than SC in both breeds, which suggests that PNS may be a better indicator trait than SC for improving female reproduction in tropical breeds in Northern Australia. Currently, PNS is included in the BREEDPLAN evaluation of Brahman cattle, with the opportunity for it to be rolled out in other tropical breeds as sufficient data becomes available. Similarly in sheep, scrotal circumference measures are used in the genetic evaluation for reproductive traits of ewes.
- **Genetics of preputial eversion in tropical breeds:** Preputial eversion (PEV) describes a defect of male reproductive anatomy, and is easy to observe and record, compared to current male and female reproduction traits. Wolcott and Johnston (2017) showed the trait was moderately heritable in Brahman males at 12, 18 and 24 months of age ($h^2 \sim 0.3$) and that genetic correlations with female age at puberty, lactation anoestrous and lifetime annual weaning rate were stronger from records from older bulls at 18 and 24 months of age. Compared to female reproduction traits, preputial eversion is easy to measure, and this study suggested it would be a useful trait to add to the genetic evaluation for tropical breeds if recording was embraced by industry.
- **Genetic association between days to calving and other male and female reproductive traits in Brahman cattle (Johnston and Moore 2019):** The Brahman evaluation now produces EBVs for days to calving (DC), age at puberty (AP) and lactation anoestrous interval (LAI). As discussed above, DC using repeat records (DCr) was further considered as separate DC traits for first (DC1) and second parity (DC2) records, as well as a simple binary trait for

calving rate (CR). Additional research has been undertaken to understand the genetic relationships of currently analysed male reproduction traits (scrotal circumference (SC) and percent normal sperm (PNS)) with these more refined descriptors of female reproduction. Heritability estimates for DCr, CR, DC1, DC2, AP, LAI, SC and PNS, were 0.09, 0.10, 0.09, 0.15, 0.47, 0.40, 0.44 and 0.15, respectively. Genetic correlations between DC1 and AP, LAI, SC and PNS were 0.62, 0.52, -0.32 and -0.66, respectively. For DC2, the genetic correlation with DC1, AP, LAI, SC and PNS were 0.46, 0.56, 1.0, -0.29 and -0.71, respectively. The study has shown that the reproduction traits examined were heritable. The moderate genetic correlation between DC1 and DC2 (0.46) suggests they should be considered as separate traits in genetic evaluation, and this would allow fitting different genetic correlations with other male and female reproduction traits. Improvement of the genetic evaluation will increase accuracies of female reproduction EBVs and allow more genetic progress in tropical beef breeds in northern Australia and is a topic of ongoing research for those breeds.

- **Combining conception rate to artificial insemination in heifers with days to calving in the Angus BREEDPLAN evaluation:** Genetic parameters for calving success to first service (CSF) by AI were estimated. Mean CSF was 56.9% with estimated heritability of 0.10. Genetic correlations estimated between CSF and days to calving measured for first mating (DCF), second mating (DCS) and third mating (DCT) were -0.12, -0.13 and -0.17 respectively and for all DTC records in the BREEDPLAN evaluation was -0.32. The genetic correlations estimated between CSF of AI and DC of NM were significantly lower than 1 and suggest that they are two different traits. Therefore, including reproductive data from both mating types in the genetic evaluation will enable greater genetic improvement of heifer fertility in Angus cattle.

Based on this R&D program, a new module for genetic evaluation of reproductive traits in beef breeds is under development. Currently, days to calving records from natural mating (DTC) is being analysed as a repeated record, with the maximum of 6 records per cow. To increase the accuracy of prediction for this lowly heritable fertility trait, the current DTC records have been split into 3 different DTC traits and combined with scrotal measurement, percentage normal sperm, age at puberty, lactation anoestrous interval and categorical trait of conception rate to artificial insemination (AI) in heifers in a mixed model evaluation. Software required to generate trial EBVs for conception rate in heifers is being developed. The new module will also be tested using Angus, Hereford and Brahman data.

5.4 Genetics of cow body composition in beef breeds

Research was undertaken to develop a new trait, predicted cow body composition, which describes the trait as body composition of lactating females entering their second mating (PM2BCS). This time-point has previously been established as the stage at which cows face the greatest demands on their energy reserves to lactate, continue to gain weight and height, and be in adequate condition to reconceive. For Brahmans, data from the Beef CRC and Repronomics^{TM} projects have been combined to predict the phenotype of lactating cow body composition at mating two, based on records of cow condition score, weight, hip height and scanned eye muscle area and fat depth. The model fits body condition score in lactating cows at their second mating (M2) as the dependent variable, with liveweight (WT), hip height (HH) and scanned eye muscle area (EMA) and P8 fat depth (P8), and significant interactions, as predictors.

The resulting trait is expressed as a predicted body condition score but has the advantage of being genuinely continuous and exploits more objective traits in its estimation. Analytically, this is a very similar method to that employed to estimate net feed intake (NFI), though for the efficiency trait, it is the residual (individual animal deviation from the mean) which is of interest rather than the predicted term, which in the case of cow body composition will be analysed as PM2BCS. Genetic analyses of PM2BCS showed the trait to be moderately heritable (0.38) and that higher genetic PM2BCS was associated with lower lactation anestrous interval but had virtually no genetic relationship with age at puberty (genetic correlations of -0.38 and -0.03 respectively).

Development of a trial EBV is well underway for the Brahman evaluation. A program of intensive phenotyping in Angus and Hereford lactating first calf females has been undertaken in the second half of 2020 and 2021 to provide the data needed to extend the research in temperate breeds.

Implementation for tropical and temperate breeds can commence as sufficient industry data becomes available. For Brahmans, this may require recording of the trait in well described and current BREEDPLAN herds to achieve adequate reference population size (including data from R&D herds).

5.5 Lambing ease in terminal sheep breeds

Complementing the focus on female reproduction efficiency and welfare in this project a new analysis for lambing ease in terminal breeds has been developed. This new analyses includes a new data preparation pipeline and the implementation of single-step, resulting in breeding values with improved predictive ability, increased accuracy and reduced bias compared to the current analysis (Li et al. 2021a).

This analysis is scheduled for implementation for LAMBPLAN terminal breeds in 2022. Future research will be needed to develop lambing ease analyses for other evaluations, and work has begun to investigate the possibility of adding survival as a trait of the lamb to the analysis.

5.6 Calving ease in BREEDPLAN evaluations

Genetic evaluation of calving ease has been available through BREEEPDLAN for several decades but has undergone little redevelopment in that time, except for a move to multi-trait analysis with birth weight and gestation length, and more recently, inclusion of genomic information through blending. A new calving ease analysis was developed in this project featuring:

- A new analysis pipeline with updated data preparation and post-analysis processing of breeding values.
- Implementation of single-step, replacing the previous blending approach to use genomic information.
- Introduction of genetic groups bringing the analysis in line with all other BREEDPLAN traits.
- Improved fixed effect modelling with re-definition of contemporary groups and direct fitting of sex and age-of-dam effects.

The developments have greatly improved the computational efficiency and accuracy of calving ease breeding values. The new analysis has been applied in Angus.

5.7 Updates to genetic parameters for BREEDPLAN evaluations

Regular estimation of breed specific genetic parameters is important to ensure the predictability of breeding values. These estimates are influenced by the amount of data along with data structure. Enrolment of new herds into evaluations and increased levels of recording leads to changes in the data structure for each breed. These changes may require the development of new models for the estimation of fixed effects and random effects to separate genetic effects from environmental influence. Therefore, identifying the changes in the data structure, developing new models to estimate genetic and non-genetic parameters and testing the impact of the newly developed parameters on genetic improvement are, thereby, an integral part of the ongoing research and developmental activities undertaken during this project.

Redevelopment of the genetic evaluation for Hereford, Angus, Wagyu and for PHA Shorthorn were undertaken. The current parameters and adjustment factors used in the Angus evaluation were estimated prior to 2012. Therefore, a major upgrade of the Angus BREEDPLAN was undertaken to re-estimate the genetic parameters and adjustment factors for the existing 26 traits and for two new traits, shear force and MSA marble score. New parameters including heritabilities and genetic correlations were estimated for the 28 traits and their pairwise combinations using a subset of Angus database with 466,579 growth, 126,055 scan, 84,899 reproduction and 13,253 abattoir carcase records. Estimated heritabilities and correlations for all were very similar to the values used in the current BREEDPLAN evaluation, except for the carcase traits. Newly estimated genetic parameters were higher than the values used in the current evaluation.

Major upgrade of the Wagyu evaluation was undertaken in 2018 and in 2021 after substantial increases in carcase records and the inclusion of camera carcase traits. New parameters (i.e. variances, heritabilities, and correlations) were estimated for 10 traits and their pairwise combinations using a subset of Wagyu database with 6,600 to 13,300 carcase traits (carcase weight, carcase rump fat, carcase eye muscle area and AusMeat marble score), 1,200 to 2,500 old camera traits (camera eye muscle area, camera marbling percentage and camera fineness index) and 710 to 980 new camera (MIJ30) traits (camera eye muscle area, camera marbling percentage and camera fineness index). Estimated genetic variances and heritabilities for the four carcase traits were higher than the previous estimates. However, the estimated heritabilities for the two marble traits, measured using the new camera, were unrealistically high and need further investigation.

6. New breeding objectives and indexes

6.1 Sheep Genetics

Indexes for several industry breeding objectives were developed, including:

- **Terminal Carcase Production (TCP):** this index was introduced in 2019 as a replacement for the Carcase+ index and compliments the Eating Quality (EQ) and Lamb Eating Quality (LEQ) indexes. Whereas EQ and LEQ target high responses in eating quality, TCP has greater emphasis on increasing lean meat yield while maintaining or slightly improving eating quality. By contrast selection on Carcase+ has led to reductions in eating quality over time. A modification to TCP to limit increasing birth weight impacting on lambing ease is planned for introduction in 2022.

- **Maternal Wool Production (MWP+):** developed in 2019 in consultation with Corriedale breeders to support self-replacing maternal breeds with a wool focus.
- **Maternal$:** updated maternal breed index introduced in 2018.

Custom indexes were also developed for several Merino breeders. Of particular note was a modification of the Merino Production (MP+) index to include emphasis to reduce breech wrinkle. This index is of general interest to complement the industry welfare issues of reducing the incidence of fly strike and elimination of mulesing.

An industry review of indexes by Sheep Genetics in 2021 has also identified easy care and resilience attributes as priorities for inclusion, along with reproduction component traits.

Revised methodology and documentation for describing standard indexes was released in 2019, developed jointly by Sheep Genetics and AGBU, with industry consultation. There are versions for ram breeders and ram buyers, and although there is a large degree of consistency, breeder versions focus more on the impacts of selection using an index, and the buyer versions focus more on how to choose an index to aid in purchasing rams using a decision tree approach.

This new approach values the contribution of traits to indexes using the concept of “Selection Advantage” calculated based on superiority of highly ranked real animals, rather than using predictions based on selection index theory. Selection Advantage has the benefit of showing the impact of using an index on real situations, capturing the variation existing among selection candidates.

Associated with this work on updating index documentation for breeders and buyers, a software tool was developed has enabled a range of comparisons and diagnostics with the aims of increasing understanding of indexes and validating predicted and realised selection responses (for example see Swan et al. (2017)). These include:

- Predictions of responses to index selection within and across indexes, accommodating different scenarios of traits recorded, generation interval and selection intensity, and use of genomic information.
- Comparison of predicted and realised genetic trends for individual flocks, leading flocks, and averaged across all member flocks.
- Comparison of rate of progress with current index mean by flock.

The tool was used regularly by AGBU and Sheep Genetics staff, working with breeders in the development of custom indexes and review of breeding programs, as outlined in Section 1.1.

6.2 BREEDOBJECT

The developments necessary to address some of the key challenges for the future Australia beef industry through genetic selection were finalised to allow implementation of the upgraded version 6 BreedObject index software. The major upgrades included a much higher focus on on-farm feed costs, primarily around the cow herd (including cow welfare as described by cow body composition; BCS) but also in the young growing animal. Simultaneously the ability to cost greenhouse gas production was established through selection for beef cattle with lower methane emissions (Barwick et al. 2019b). Also developed was the capacity to construct multi-breed indexes when multi-breed EBVs available (Barwick et al. 2019a).

Other useful and industry-relevant developments included the capacity to use non-linear cost structures such as carcase grids for calculating economic values. Where appropriate the capacity to have non-linear economic values for all breeding objective traits, and the capacity to differentiate the value of cull cows based on the reasons the cow is culled from the herd (e.g. reproductive failure, structure, temperament) were also developed.

These upgrades were implemented in the BreedObject website in October 2016 and made available to ABRI for inclusion in the BREEDPLAN evaluation pipeline in late 2016. This has allowed ABRI to deliver version 6 BreedObject indexes for testing and routine implementation in a timelier manner. As part of the delivery of the upgraded software an initial implementation meeting was held with ABRI and breed society participants, followed by specific meetings with different users to address specific questions or to facilitate use of the BreedObject website. These meetings have acted as an important mechanism to receive feedback and address software issues identified by index developers and users. These issues were addressed and implemented throughout 2017 and 2018.

The implementation of new indexes by breed societies has involved a considerable extension effort. Extensive consultations have been conducted with breed society boards and consultation committees both in association with and independent of ABRI. These activities have been highly valuable in increasing the knowledge base of staff, board and committee members and has improved their understanding of the advancements in the BreedObject indexing technology, which has improved adoption. This groundwork will be particularly valuable in the future as addressing the cost of production around the feed requirements of livestock is the first step in addressing greenhouse gas production. Extensive consultation has been conducted with the Australian Wagyu, Hereford and Angus societies while smaller consultation has been had with the Murray Grey, Charolais, Limousin and Belmont Red societies and the Performance Herds Australia group.

New indexes were implemented for the Australian Wagyu, Hereford, Limousin, Charolais and Belmont Red breeds and the Performance Herds Australia group. New indexes are at various stages of development for the Australian Angus, Red Angus, Murray Grey, Droughtmaster, Simmental, South Devon, Brahman, Brangus and Santa Gertrudis breeds with some being close to implementation. Customised indexes have also been developed and implemented for several Australian pastoral companies including NAPCO, Te Mania, Twynam, Kaiuroo and Wambiana Station. Enquiry has also been received from and interactions have occurred with other parties considering the use of customised indexes.

Overall, the extensive consultation around indexes with breeds and breeders is judged to have increased industry confidence in the BREEDOBJECT tool and has involved significantly greater direct engagement with the users than was the case with earlier index upgrades. While this has represented a considerable time commitment, it has led to a much greater sense of ownership of indexes by the breeds and breeders, anticipated to lead to more focus on indexes in selection and marketing.

7. Adoption activities

1.1 Sheep

Throughout the life of this project, AGBU has contributed to a range of extension and adoption activities. These have ranged from supporting Sheep Genetics with material and tools, through to assisting with delivery of information at industry events. The primary roles in these activities have centred around describing the R&D and its implications for breeders, and also to provide independent and objective breeding program advice for industry. These activities have included:

- **Development of extension material:** AGBU have assisted with the development of written materials, such as the Breeder's Manual, Breeder's Bulletin articles, information sheets, press releases and index documentation. The team has also helped create and record several video and recorded webinars for breeders. AGBU also supported the MLA genetics adoption campaign with technical review and input in the materials developed.
- **Decision support tools:** AGBU has developed a number of new tools throughout the project that were used extensively to provide material for workshops and to underpin advice to breeders. These include Ramping-Up Genetic Gains analysis system, comparative analysis of genetic progress, and breeding program design tools (described above in 0). These tools were used to develop material and present at workshops.
- **Presentations and attendance at workshops and industry events:** AGBU staff have assisted with the delivery of numerous Sheep Genetics events. These have included Leading Breeder conferences, service provider training, software provider workshops, regional forums, MateSel training workshops, ultrasound scanner accreditation workshops, breeder performance groups, other groups such as AMSEA and MerinoLink, and other field days. The team has also participated in numerous industry events such as Bendigo Sheep Show, SheepVention, LambEx, AMSEA, AAABG, WCGALP and ASAP.
- **Contributions to the governance process behind Sheep Genetics and the AGBU workplan:** AGBU staff have played a key role in the development, review and implementation of the annual operational plans behind the development of the Sheep Genetics evaluation. This involved regular participation in and presentation to the Sheep Genetics Executive, Advisory and Technical committees.
- **International collaboration and scientific communication:** Communication with scientists and breeders from across the world is important for AGBU to keep up to date with technological changes and also to encourage thorough peer review of the Sheep Genetics evaluation. AGBU have been involved in a number of international events, conferences and other meetings throughout the project.
- **Technical advice:** Another key role for AGBU is to provide technical advice to breeders, genetics service providers, research and industry groups. As such, AGBU has had many roles on committees and groups such as AMSEA executive, MSA pathways, NLGC taskforce, ALMTech calibration working group, CRC Information Nucleus and MLA Resource Flock oversight committees, other research groups, and ICAR. In addition, there have been many regular one-on-one interactions to share information and provide advice.

Data quality in sheep evaluations has been a key focus during this project. Ramping-Up Genetic Gains reports were a key element of discussion with all breeders and groups. This analysis tool, and the reports built from it, were improved significantly throughout the project. This also led to the completion of the Data Quality Score system which was developed and road-tested through the companion project (L.GEN.2004). Additional analysis reports were also built using these data and used every year of the project with all the breeder performance groups and at MerinoLink project meetings.

This project also contributed advice provided to the MerinoLink DNA stimulation project (MLA P.PSH.0961) which focused on assisting Merino ram breeders and commercial producers in the adoption of genomic tools and improving data quality and accuracy of ASBVs. The project has had a major impact on the growth of genotyping in the Merino evaluation (see **Figure 1**), and has substantially increased rates of genetic gain in the participating ram breeder flocks (Martin and Granleese 2021).

In collaboration with Sheep Genetics, consultation with stakeholders is a key part of AGBU's role. This has also been a critical part of this project and not only helps AGBU and Sheep Genetics develop well-focused work plans, but it also assists breeders understand what AGBU does and the complexities of R&D in genetic evaluation.

These industry interactions have had a demonstrable impact on industry practices, improved breeding programs, and genetic gain, for example:

- Merino ram breeders in MerinoLink DNA stimulation project on target to double rates of genetic gain by 2022 using genomic tools underpinned by the single-step evaluation developed in this project.
- Working with young sire programs in terminal sire breeds assisted with the adoption of breeding objectives focusing on lamb eating quality, along with breeding program strategies to increase accuracy, resulting in measurable genetic improvements in these traits (see **Figure 2**).
- During the development of the new reproduction breeding values, workshops with leading maternal sheep breeders were critical to creating understanding, improved recording, and acceptance of a major change. In addition, working with these breeders to genotype breeding ewes has generated a substantial distributed genomic reference population for these traits.

7.2 Beef

The focus for extension was to engage with influential seedstock breeders and their representative bodies, with strategic inclusion of large commercial breeding enterprises, where the investment was expected to generate real practice change and genetic progress for economically important traits. Engagement with breed societies maintained a focus on detailed evaluations of breed level genetic trends and recording practices, following an established but evolving 'Breed Audit' format. These highlighted opportunities for breeds to promote phenotyping strategies to their members to address deficiencies in current data submitted for evaluation, and to present opportunities to include new traits in their recording program to address economically based breeding objectives.

A key topic for engagement with breeders and breed societies was discussion around the opportunities presented by the single-step evaluation. Advice on genotyping strategies formed a significant part of these interactions, and the resulting uptake of the technology has seen increases in EBV accuracy for animals related to their respective breed reference populations. The introduction of single-step has also made it possible for genetic benchmarking of animals which previously were ineligible to have BREEDPLAN EBVs published. The contribution to adoption of this new technology made by AGBU's beef extension and engagement program is a key outcome for this project.

Another important component of engagement for AGBU within the current contract has been the introduction of breeders, and their representative bodies, to new traits developed for their evaluations. This has been particularly so for tropical breeds, with the introduction to their evaluations of reference and industry-based recording of more precise, and significantly more heritable, female and male reproduction traits (age at puberty (AP), lactation anoestrous interval

(LAI) and percent normal sperm (PNS)). How these new records impact on the evaluation for tropical breeds, and how breeders could best exploit the new information, was a focus of extension efforts as the traits were rolled out. Brahman breeders were the first to be able to access the new reproduction traits, and the level of recording (both in research and industry herds) and subsequent selection has resulted in clear improvements in genetic trends since their introduction.

In 2020, the impossibility of face-to-face interaction (due to COVID) required a change to more remote, on-line interaction by video conferencing. This format was not suitable for in-depth discussion of individual breeding programs, and the focus shifted to maintaining contact around developments to the evaluation and saw an added focus on train-the-trainer activities and remote, group interaction. These aimed to improve awareness and understanding of ideas underpinning genetic evaluation and the tools available to beef breeders to maximise the impact of these on their breeding programs. A focus of this work was the SBTS-managed Beef Champions network, which provides a forum to present to stakeholders including beef genetics extension specialists and service providers. Presentations to this group from 2018 to 2021 have sought to improve understanding of the mechanisms underlying BREEDPLAN genetic evaluations, and to keep the group informed of current areas of research at AGBU.

The AGBU beef project has also seen significant engagement with the Australian and international scientific community. Presentation of results at scientific conferences and breeder meetings with a focus on cutting edge research (such as the BIF conference in the US) have been an important feature of AGBU engagement over the last five years. This has seen presentations of new results around opportunities to improve beef genetic evaluation at biennial AAABG conferences (2017, 2019 and 2021) and the important quadrennial meeting of the WCGALP (held most recently in Auckland in 2018). There has also been regular engagement with international breeder and breed representative groups in a range of areas to improve understanding of world class research around genetic evaluation and its implementation. This has included interaction with breeders in the US, South (and southern) Africa, Great Britain, Ireland, and others. This interaction is almost exclusively by invitation from international breeders and their representative bodies, many of whom are BREEDPLAN clients, and maintains the profile of AGBU research as providing world leading genetic evaluation tools to industry.

In 2020 and 2021 AGBU has undertaken strategic phenotyping with the beef activities of this project to rapidly generate phenotypes for new traits to describe lactating cow body composition in temperate beef breeds (see Section 0). This work has involved engagement with key Angus and Hereford seedstock breeders, and the opportunity to discuss recent and emerging areas of research has been a small, but extremely useful form of engagement. Addressing questions breeders have and becoming better informed about areas of concern for some of the leading users of the BREEDPLAN product, in an informal setting, has made a useful contribution to AGBU's engagement effort.

Finally, there has been a noticeable increase over the course of this project in the interaction of AGBU beef breeding specialists with breeders, on an ad hoc basis, in the form of unscheduled phone or email contact. This is likely a result of greater exposure on persistent web-based media, such as the SBTS workshop series, FutureBeef webinars, BIF conference presentations uploaded to YouTube, and the Te Mania RawAg podcast series. These interactions can range from brief discussions to enquiries which require analyses and interpretation of results. These go largely unreported and un-budgeted for in work planning, but represent an important, and not insignificant, element of the engagement and contribution to industry adoption.

8. Benefits to Industry

Key developments delivering benefit to industry include:

a) Enabling implementation of genomics across a wide range of breeds, all traits, at a scale that is growing exponentially. This is enabling earlier selection, more precise steering of the breeding program, and scope for wide-scale screening of commercial animals, which is starting to radically transform value chain relationships and management.
b) Simpler genetic evaluation for extensive systems via DNA testing, enabling much greater adoption of EBVs and ASBVs in northern cattle and Merinos respectively, enabling step change in productivity and profitability in those sectors.
c) Scope for significant and rapid improvement in branding rate in northern cattle through an expanded suite of EBVs for fertility traits.
d) Scope for more precise control of improvement in reproduction in sheep, avoiding potential welfare catastrophes arising from fecundity outpacing survival.
e) EBVs for traits related to welfare in both species, an example being the improved analysis model for calving ease, which extracts more information from typical industry data and enables more accurate selection and hence more rapid reduction in calving difficulty.
f) Breaking the nexus between efficiency and product quality in sheep meat production – allowing the Australian industry to move to a level of product quality beyond any competitors without sacrificing cost efficiency.
g) Understanding the relationships between MSA traits and production traits in beef cattle, enabling a similar step change for the beef industry.
h) Extension of the range of carcase traits in beef stimulating increased focus on product quality.
i) Improved modelling of feed cost in cattle systems setting a platform for much greater focus on efficiency, and the ability to reduce carbon/methane emissions rapidly and in economic balance with other traits influencing value chain profit.
j) And considerable input to industry extension around utilisation of genomic technologies, at both the herd or flock, and breed, levels. This is helping to accelerate use of these technologies, and changes in investment patterns at both levels. These changes will lead to significant structural change in industry, and we can be confident that the changes will include greater focus on collection of phenotypes for valuable traits, wider use of elite sires through AI, systematic integration of genomics and reproductive technologies to multiply elite genetics and accelerate genetic progress, and likely emergence of much larger breeding businesses.

Overall, the acceleration potential through genomics guided by comprehensive trait coverage establishes the foundation for widespread change across the industries.

There are signs that this is underway even through the period of this project. The following tables capture the key elements of the impact of genetic evaluation and improvement – the numbers being evaluated per year, and the rate of progress in $Index units. In beef (**Error! Reference source not found.**) the data show similar numbers of animals entering evaluation in the 3 categories, but very significant increases in rates of genetic progress in British and Tropical breeds, resulting in a 36% overall increase in impact. A lot of this increase has occurred through gains in the tropical beef sector.

Table 4: BREEDPLAN Impact Statistics 2011-2015 and 2016-2020 (weighted within category)

Time Period	Number of new animals evaluated per year			Average Index Trend ($ per cow joined per year)			Impact - #s x index trend weighted sum
	British	Tropical	European	British	Tropical	European	
2011-2015	114,297	25,357	21,811	3.95	0.85	1.91	513,971
2016-2020	113,554	25,200	18,713	5.44	1.67	1.98	696,468
ratio	99%	99%	86%	138%	196%	104%	136%

Table 5: Sheep Genetics Impact Statistics 2011-2015 and 2016-2020

Time period	Number of new animals evaluated per year			Average Index trend			Impact - #s x index trend weighted sum
	Terminal	Maternal	Merino	Terminal	Maternal	Merino	
2011-2015	93,112	29,041	104,414	1.31	1.77	1.84	365,313
2016-2020	97,896	36,521	106,642	1.99	2.99	4.32	764,525
ratio	105%	126%	102%	152%	169%	235%	209%

In sheep (**Error! Reference source not found.**), the data show a marked increase in numbers of new animals annually, and large increases in rates of genetic progress in all 3 categories, resulting in an overall 209% increase in impact, which more than cover the cost of the R&D (data not shown).

9. Conclusion

This project has straddled one of the most transformative periods in livestock genetic improvement with the widespread adoption of genomic selection and the move the single-step evaluations. Australia’s national programs for sheep (Sheep Genetics) and beef (BREEDPLAN) have managed a seamless transition to the most comprehensive single-step, multiple trait evaluation for these species globally. This transition has required custom developments and technical rigour along with significant consultation. The result has been enthusiastic uptake of the technology with significant increases in rates of genotyping in both species.

Genomic selection alone will not progress the industry. For the potential benefits of genomic selection to be realized, the data recording and selection systems need to be in place to support and harness the benefits. Although the adoption of genomic selection in both species has been a huge success, the project has also progressed a comprehensive approach. With the infrastructure for genomic selection in place a doubling down of effort on improving comprehensive resource populations has been a new focus. Further development of traits related to efficiency and wellbeing are now be progressed more rapidly with genomics allowing accurate breeding values to be projected on young selection candidates. Appropriate breeding objectives and resulting indexes will allow for efficient incorporation of this ever-expanding array of traits and information, expediting progress for whole of supply chain profitability at the breeder level and allowing more informed choices for ram and bull buyers.

9.1 Key Developments

The primary overarching development has been the implementation of single-step genomic breeding values in the major analyses in both species, with more efficient computing strategies providing the basis for the rapidly expanding use of genomics.

In sheep, genomically enhanced breeding values have transformed the ability to select for lamb meat quality and female reproduction, with the latter representing a major improvement in trait definition to separate components related to reproductive efficiency and welfare.

In beef, genetic parameters for an expanded range of carcase traits for several breeds were estimated and introduced to BREEDPLAN, along with additional traits related to male and female fertility and resilience through cow body composition.

The BreedObject system upgraded to incorporate significantly enhanced modelling of feed, along with capacity to include methane costs in breeding objectives and indexes for beef cattle. All the main breeds using BREEDPLAN have developed new indexes through the upgraded BreedObject.

For sheep, important new indexes balancing eating quality and lean meat yield were introduced in terminal sire sheep and for dual-purpose maternal sheep.

9.2 Benefits to industry

This project has delivered significant developments enabling faster and more profitable genetic improvement for the beef and sheep industries, and importantly, these developments are already being implemented to encouraging extents. This immediate implementation is an important feature of the rapid R&D-to-delivery pipelines in BREEDPLAN and Sheep Genetics, and the guidance and engagement arising from the consultation processes. The increases in animals recorded and index gains noted in Section 8 signal very strong trust in the BREEDPLAN and Sheep Genetics systems, both within the seedstock sector and clients of the seedstock sector. This bodes very well for the next phase of industry utilisation of genetic evaluation and improvement technologies.

Overall, the project has delivered a relatively seamless implementation of advanced genetic analysis – the only full multi-trait single-step implementation in the world – coupled with important advances in traits being analysed. At the same time, the project, through extension activities contributed to increased utilisation of the tools. The trait analysis developments have strengthened the synergies between genetic methods and other avenues to improvement: most notably in the closer integration of meat quality (MSA and EQ traits) knowledge and data, but also in tools to tackle welfare and feed utilisation challenges. This integration across disciplines helps to maximise the cost-effectiveness of R&D in all these areas. A complementary dimension is the inclusion of traits relevant to all sectors of the value chain, providing the basis for much stronger engagement with genetics from all sectors, and stronger more value-focussed relationships between sectors.

Together, the technical rigour underpinning trust combined with innovation opening the door to massive increases in use of DNA technologies, and the ever more comprehensive coverage of efficiency, quality and social license traits across the value chains, provide the platform for widespread transformation of the red meat industries suggested above.

10. Future research and recommendations

The primary recommendations arising from the project are:

- Strong extension focussed on exploiting the opportunities created:
    - For bull and ram breeders, on topics including:
        - Optimal investment in recording and/or genotyping
        - Strong understanding of breeding objectives
        - Optimising breeding program design to exploit genomics
    - For bull and ram users, on topics including:
        - Strong understanding of breeding objectives
        - Using genetic strategies as a basis for longer-term value-based relationships with value chain partners
        - Using genomics to screen progeny to optimise alignment with management and market niches, aiming to minimise waste from use of “wrong” animals and to maximise profit generation
- Development of traits focussed on social license
- Further development of methods to use data from all possible sources – genomic sequence, own and other breeds, all sectors of the value chain, and
- Continuing development of knowledge and tools for optimising breeding program design.

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